Protein evolution in the human influenza virus

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The seasonal influenza A virus undergoes rapid evolution to escape human immune response. Adaptive changes occur primarily in antigenic epitopes, the antibody-binding domains of the viral haemagglutinin. This process involves recurrent selective sweeps, in which clusters of simultaneous nucleotide fixations in the haemagglutinin coding sequence are observed about every 4 years. I will argue that influenza A (H3N2) evolves by strong clonal interference. This mode of evolution is a red queen race between viral strains with different beneficial mutations.

Clonal interference has an important biological consequence: it tightly couples conservation and adaptation of viral functions which are encoded in linked genome sequence. Viral fitness crucially depends on antigenic adaptation, which takes place primarily by amino acid changes in antigenic epitope sites. However, it also depends on the conservation of protein stability and other functional traits, which are encoded in HA domains outside the epitopes and in other genome segments. Successful viral strains are those that maximize the total fitness of antigen-antibody interactions and of other viral functions by a joint process of adaptation and conservation. I discuss the implications of these findings for the prediction of influenza evolution.

Reference:

N. Strelkowa and M. Lässig, Clonal interference in the evolution of influenza, Genetics (2012, in press).